FIG. 1A

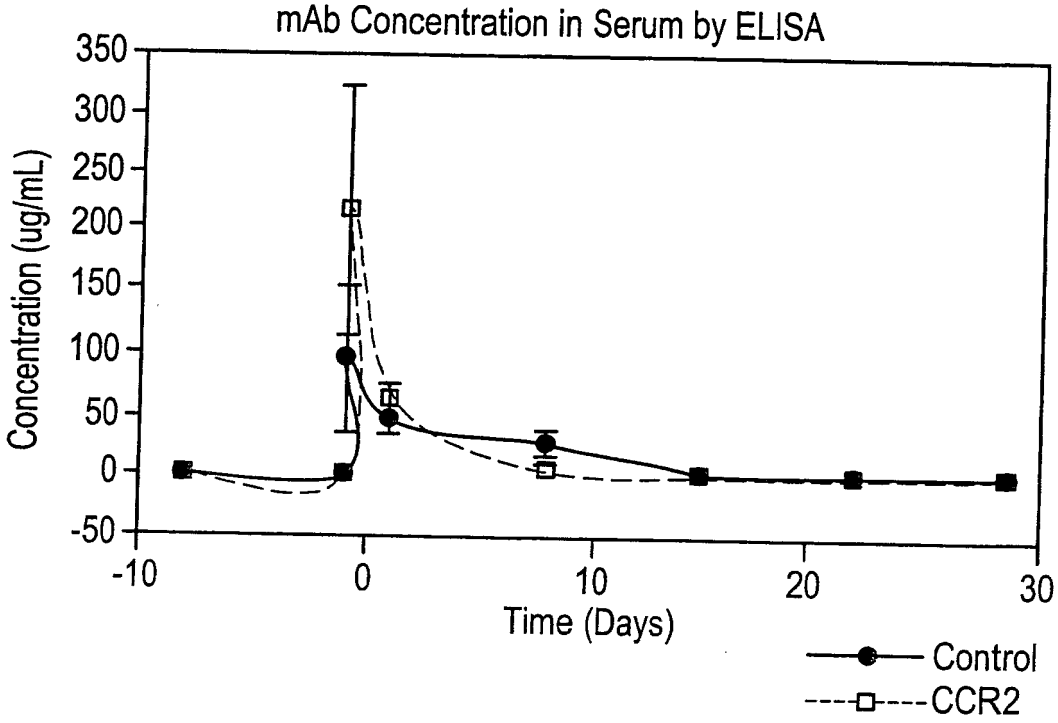

mAb Concentration in Serum by ELISA
Concentration (ug/mL)
350
300
250
200
150
100
50
0
-50
-10
0
10
20
30
Time (Days)
Control
CCR2

FIG. 1B

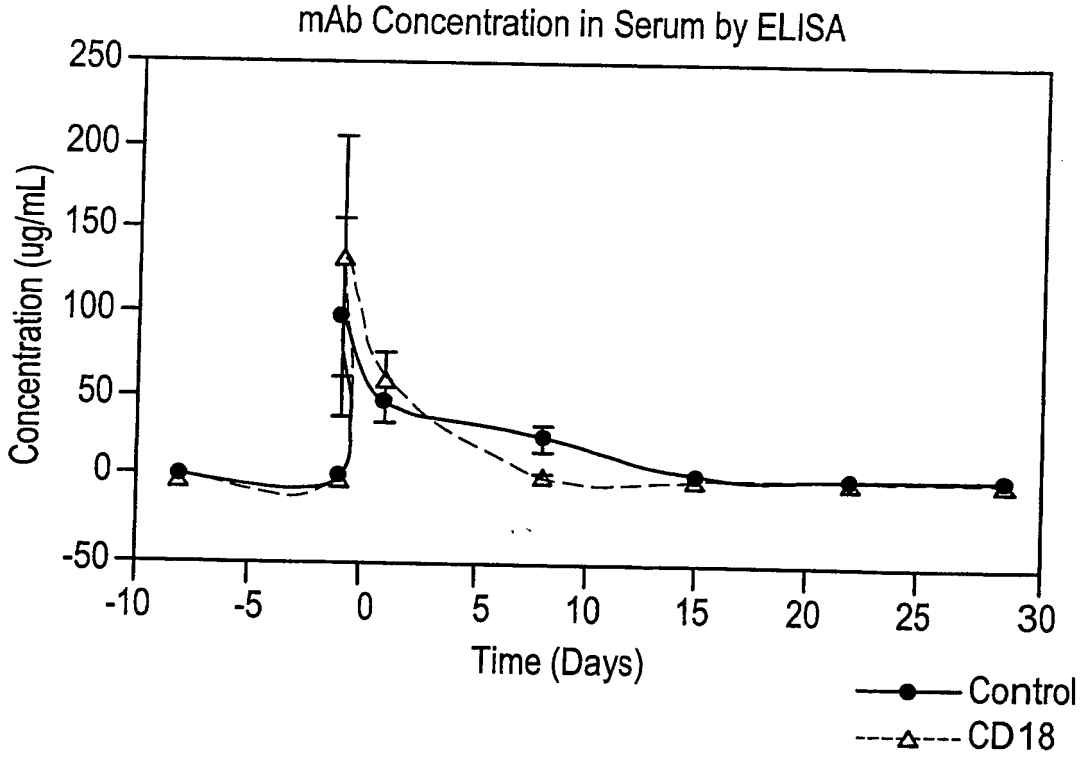

mAb Concentration in Serum by ELISA
Concentration (ug/mL)
250
200
150
100
50
0
-50
-10
-5
0
5
10
15
20
25
30
Time (Days)
Control
CD18

FIG. 2A

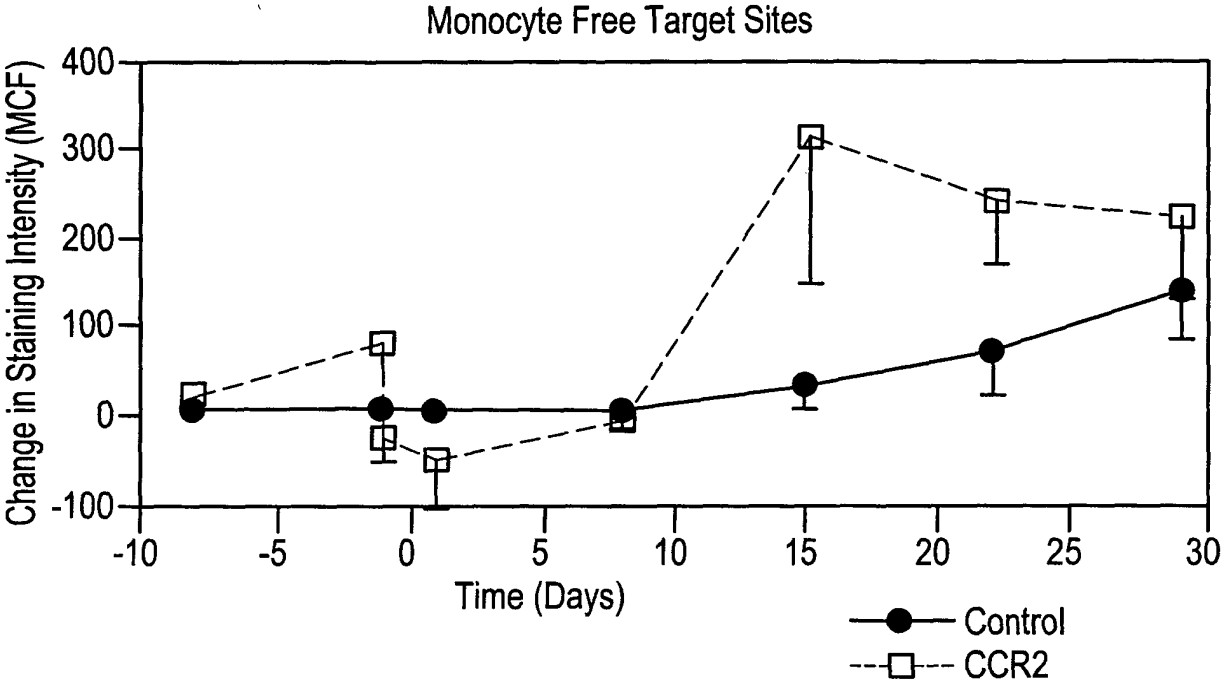

Monocyte Free Target Sites
Change in Staining Intensity (MCF)
400
300
200
100
0
-100
-10
-5
0
5
10
15
20
25
30
Time (Days)
Control
CCR2

FIG. 2B

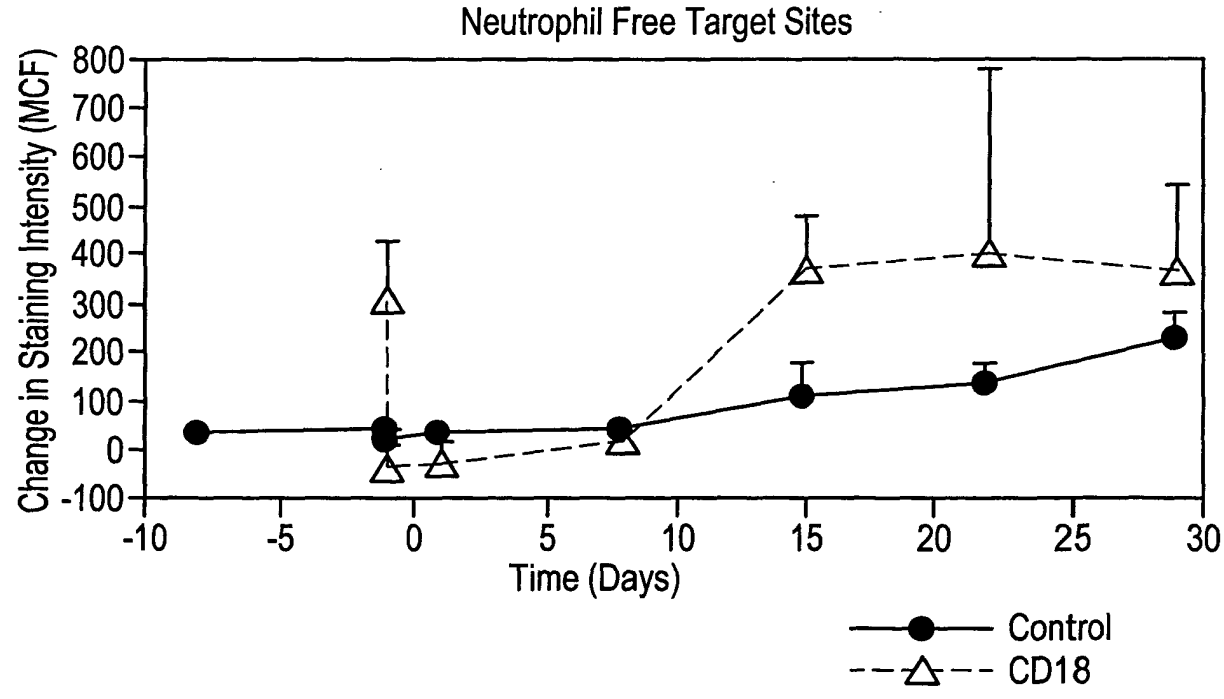

Neutrophil Free Target Sites
Change in Staining Intensity (MCF)
800
700
600
500
400
300
200
100
0
-100
-10
-5
0
5
10
15
20
25
30
Time (Days)
Control
CD18

FIG. 2C

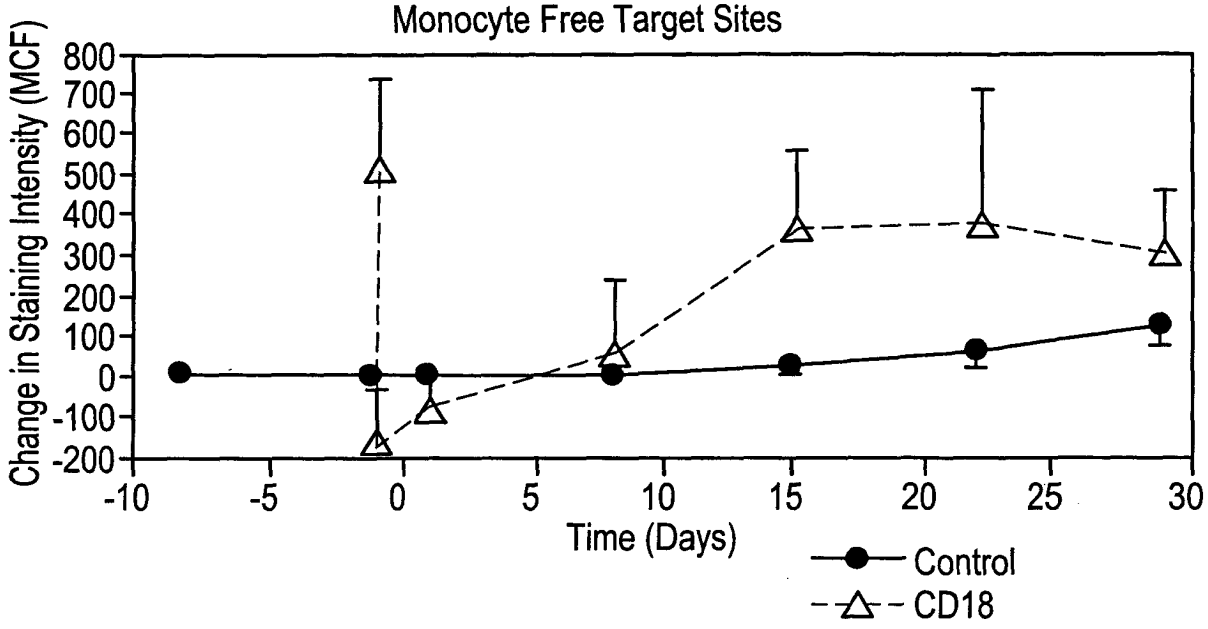

Monocyte Free Target Sites
Change in Staining Intensity (MCF)
800
700
600
500
400
300
200
100
0
-100
-200
-10
-5
0
5
10
15
20
25
30
Time (Days)
Control
CD18

FIG. 3A

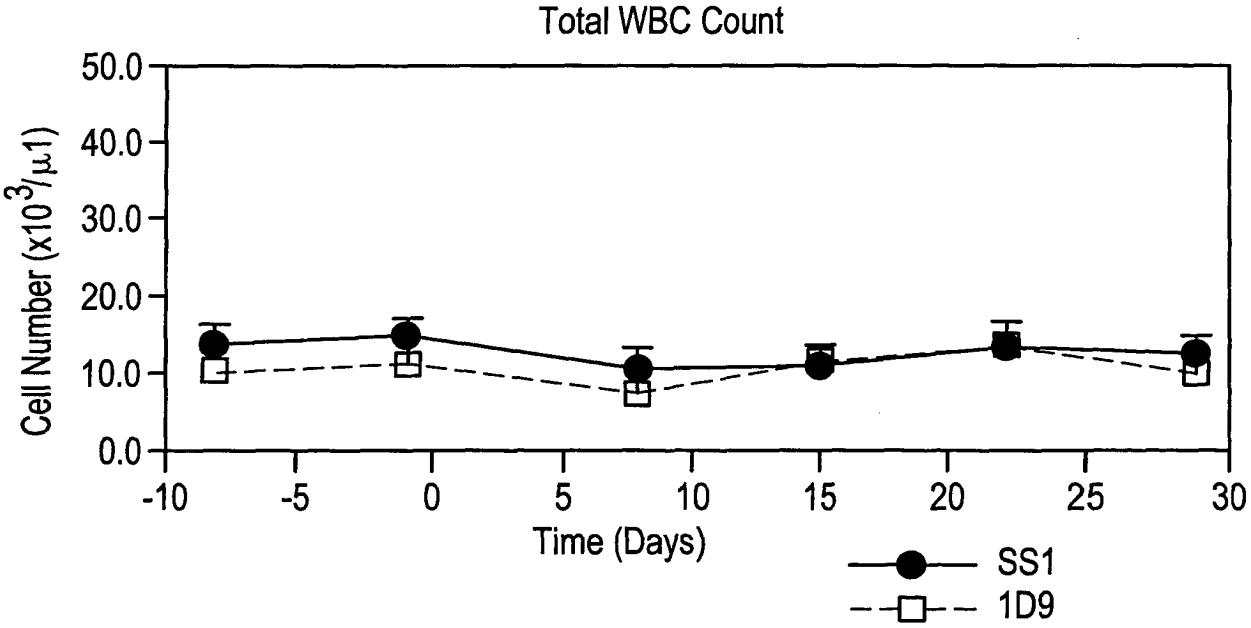

Total WBC Count
Cell Number (x10^3/μl)
50.0
40.0
30.0
20.0
10.0
0.0
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1D9

FIG. 3B

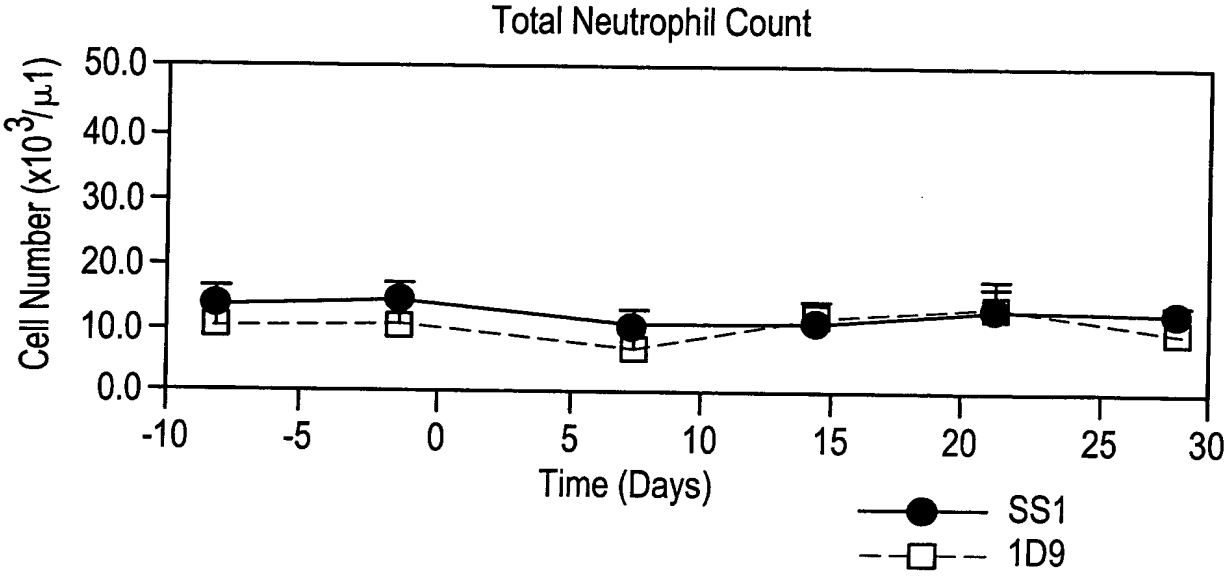

Total Neutrophil Count
Cell Number (x10^3/μ1)
50.0
40.0
30.0
20.0
10.0
0.0
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1D9

FIG. 3C

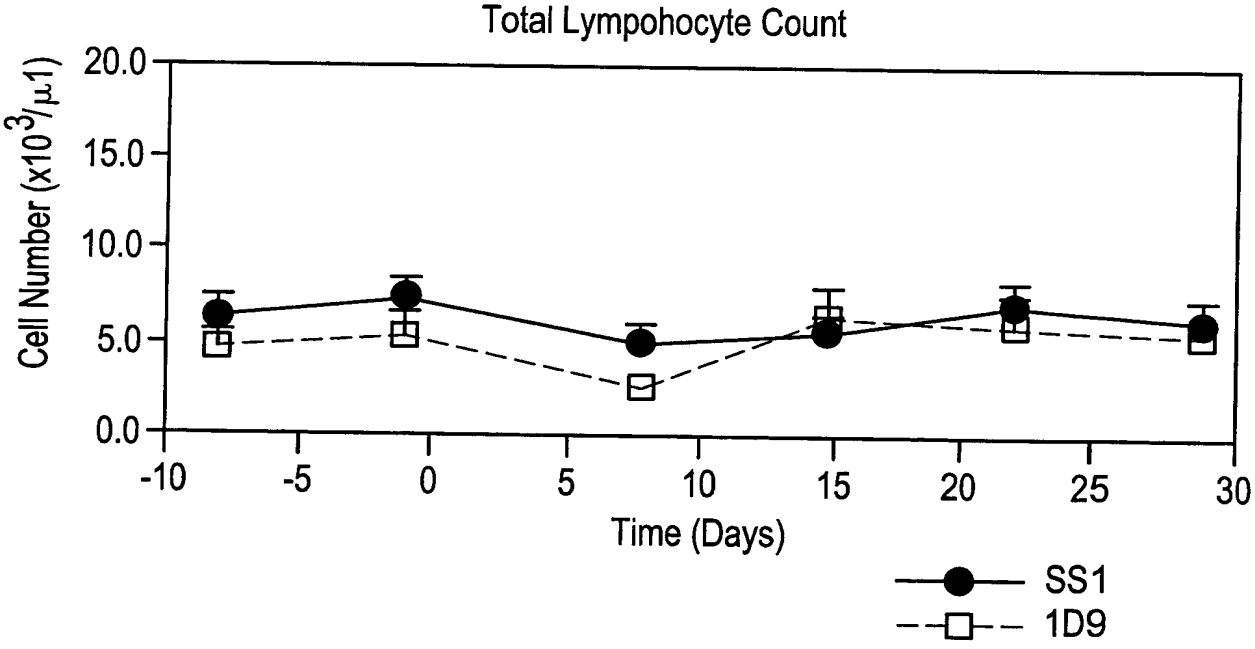

Total Lympohocyte Count
Cell Number (x10^3/μ1)
20.0
15.0
10.0
5.0
0.0
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1D9

FIG. 3D

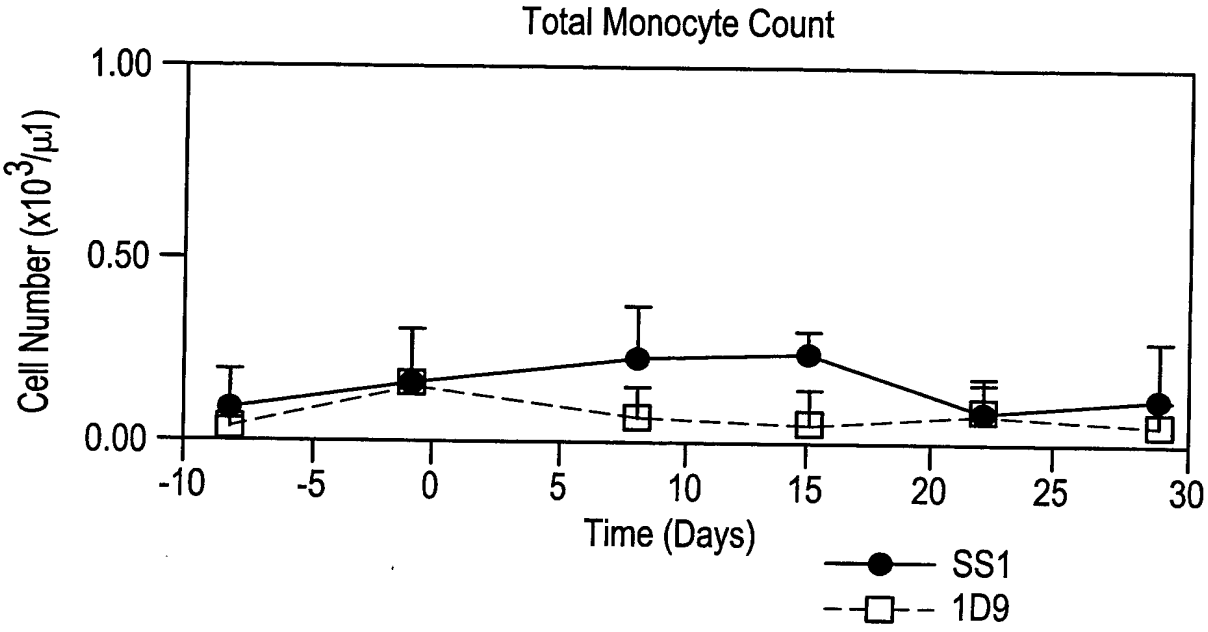

Total Monocyte Count
1.00
0.50
0.00
Cell Number (x10^3/μl)
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1D9

FIG. 3E

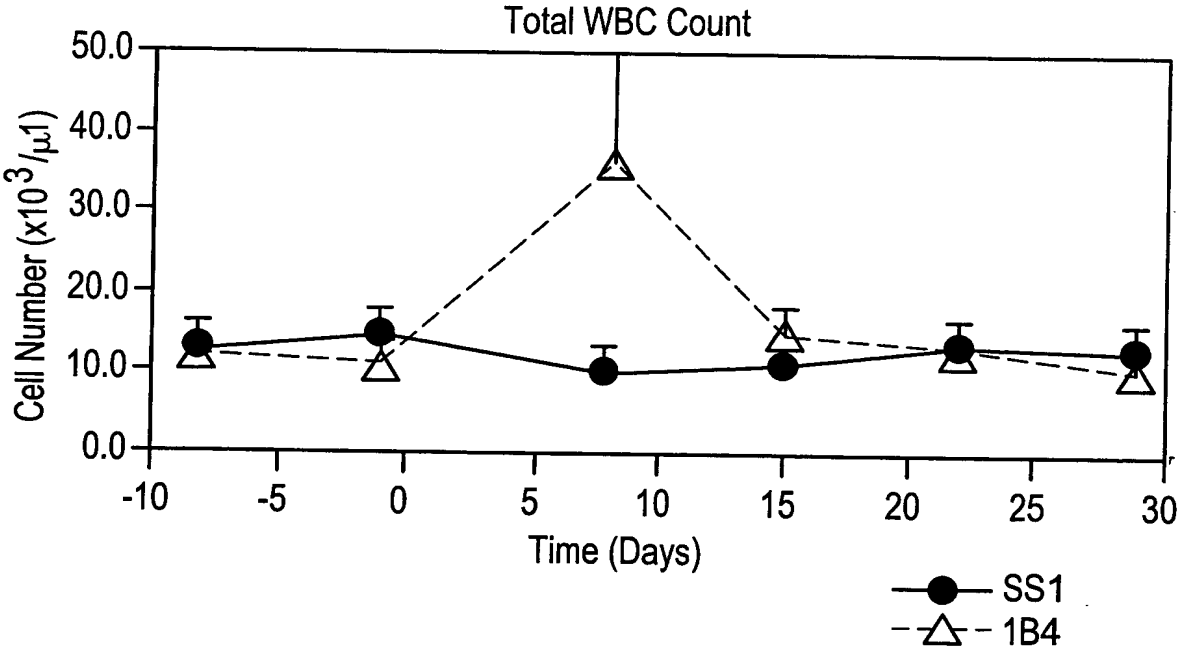

Total WBC Count
50.0
40.0
30.0
20.0
10.0
0.0
Cell Number (x10^3/μl)
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1B4

FIG. 3F

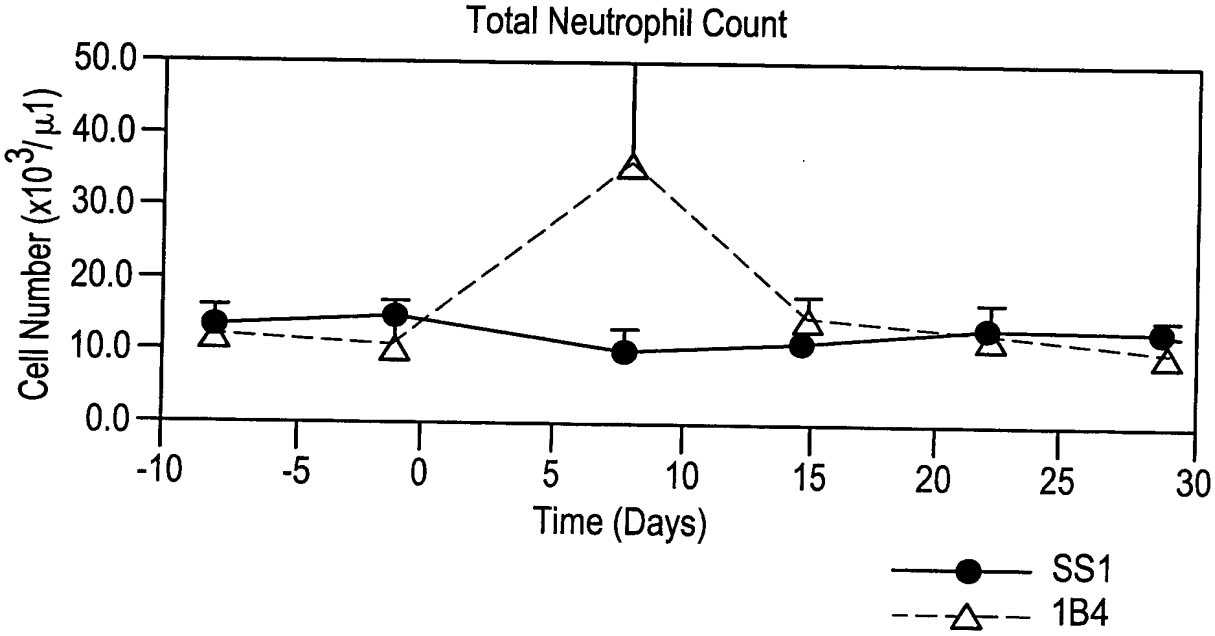

Total Neutrophil Count
Cell Number (x10^3/μ1)
50.0
40.0
30.0
20.0
10.0
0.0
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1B4

FIG. 3G

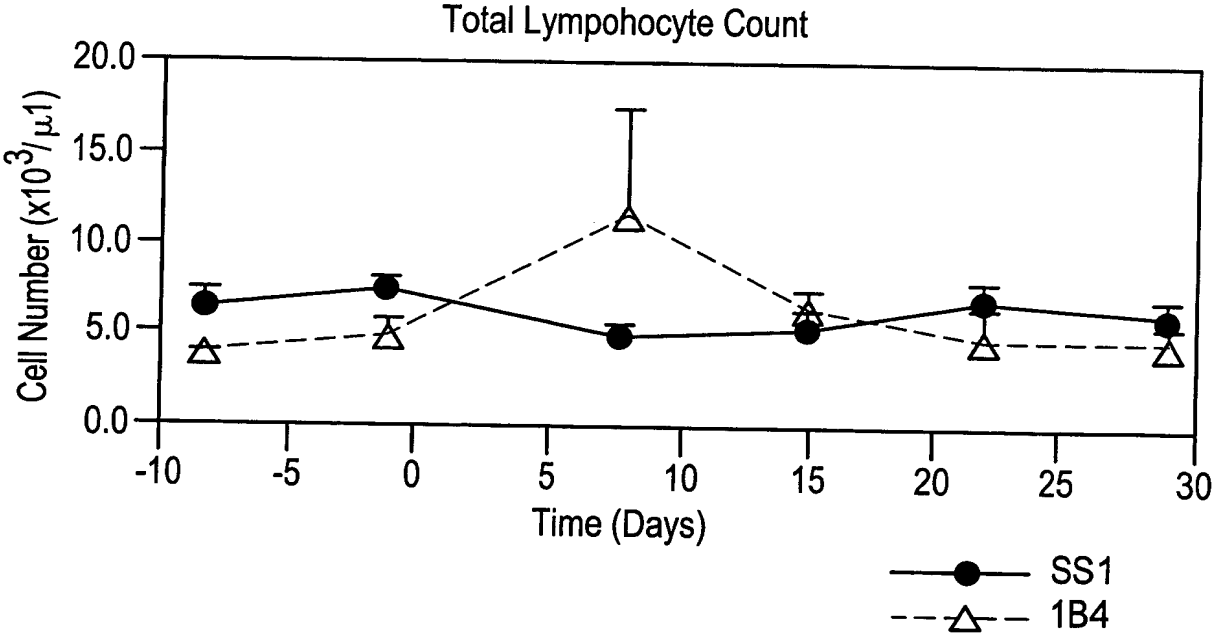

Total Lympohocyte Count
Cell Number (x10^3/μ1)
20.0
15.0
10.0
5.0
0.0
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1B4

FIG. 3H

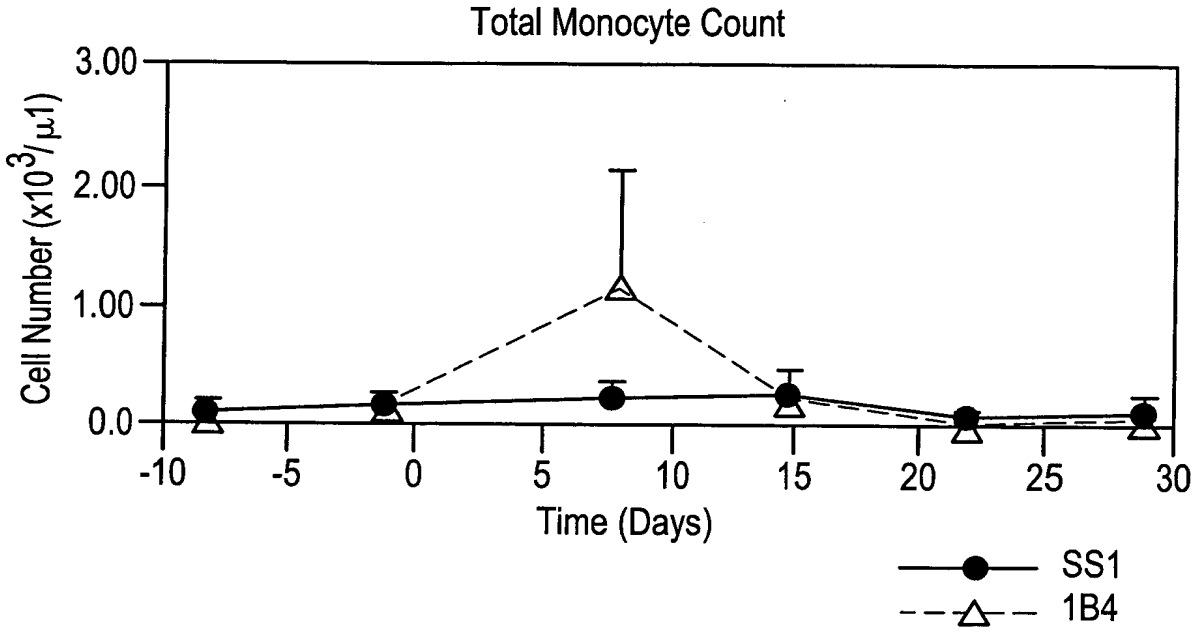

Total Monocyte Count
Cell Number (x10^3/μl)
3.00
2.00
1.00
0.0
-10
-5
0
5
10
15
20
25
30
Time (Days)
SS1
1B4

FIG. 4A

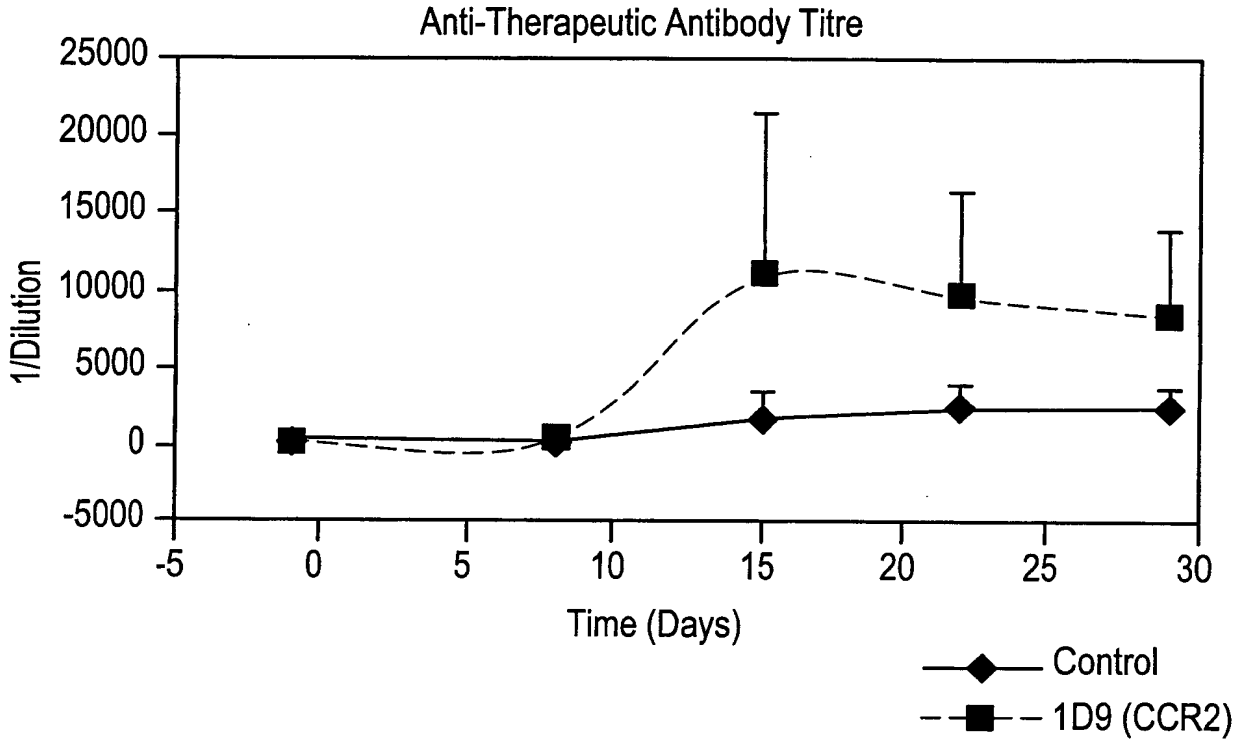

Anti-Therapeutic Antibody Titre
25000
20000
15000
10000
5000
0
-5000
1/Dilution
-5
0
5
10
15
20
25
30
Time (Days)
Control
1D9 (CCR2)

FIG. 4B

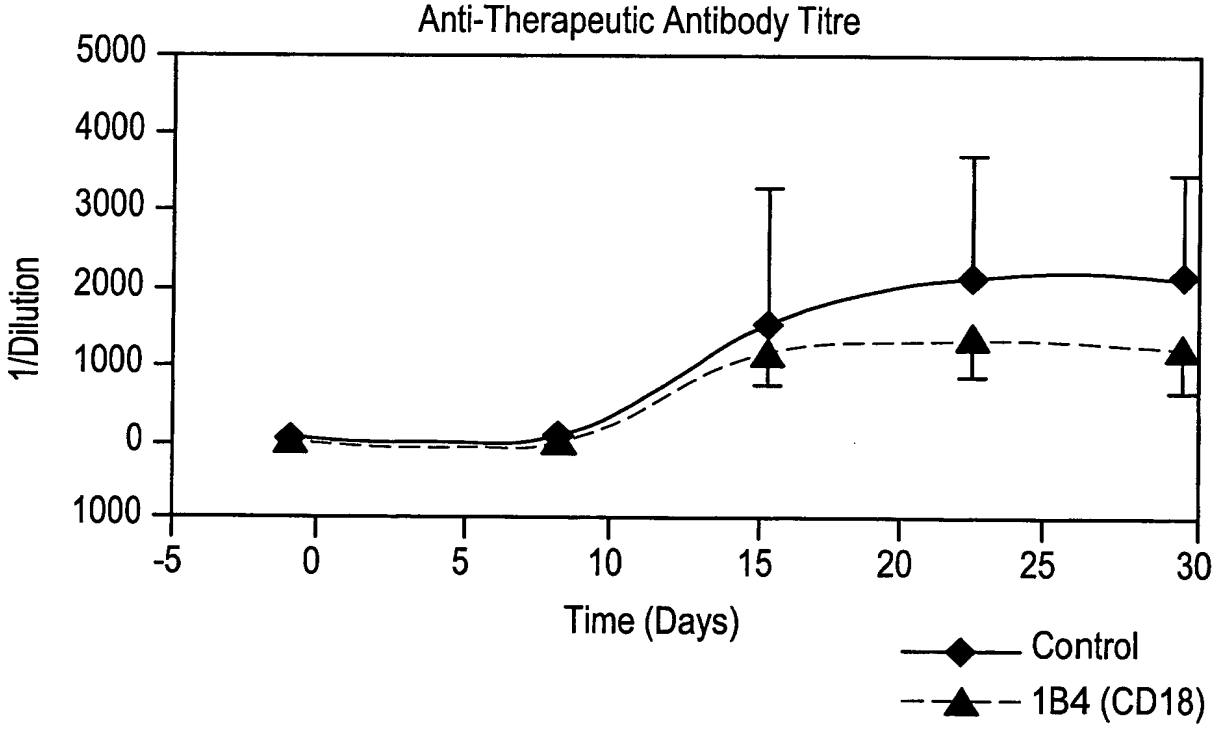

Anti-Therapeutic Antibody Titre
5000
4000
3000
2000
1000
0
1000
1/Dilution
-5
0
5
10
15
20
25
30
Time (Days)
Control
1B4 (CD18)

FIG. 5A

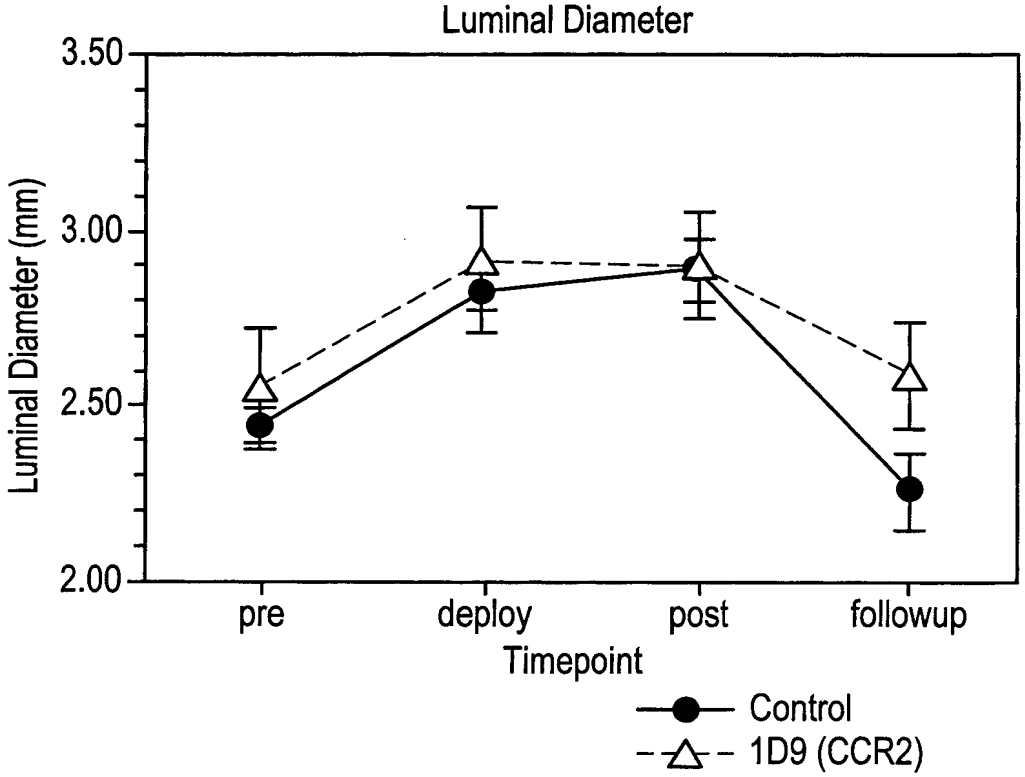

Luminal Diameter
3.50
3.00
2.50
2.00
Luminal Diameter (mm)
pre
deploy
post
followup
Timepoint
Control
1D9 (CCR2)

FIG. 5B

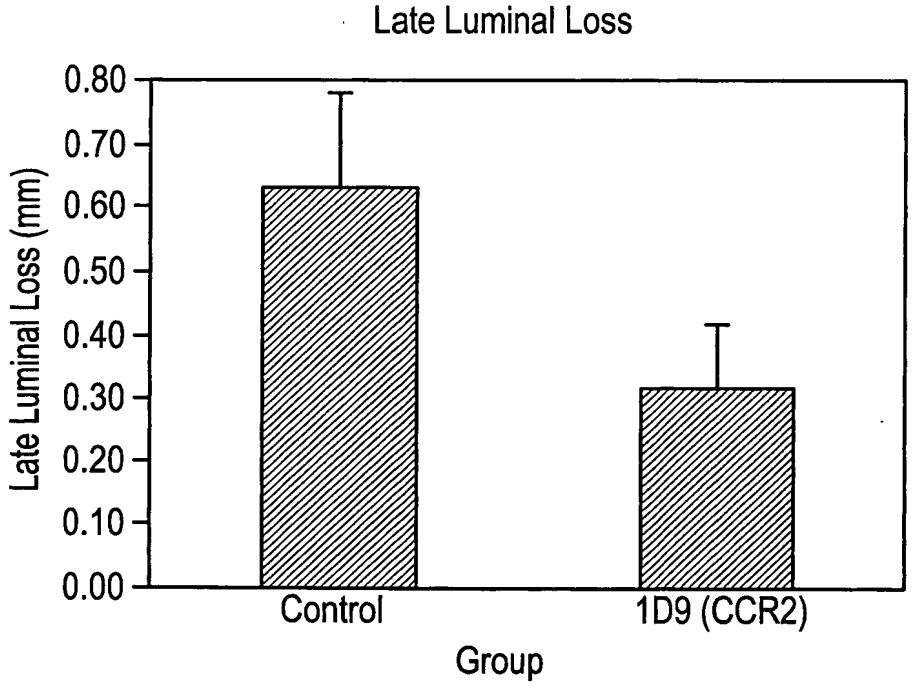

Late Luminal Loss
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
Late Luminal Loss (mm)
Control
1D9 (CCR2)
Group

FIG. 5C

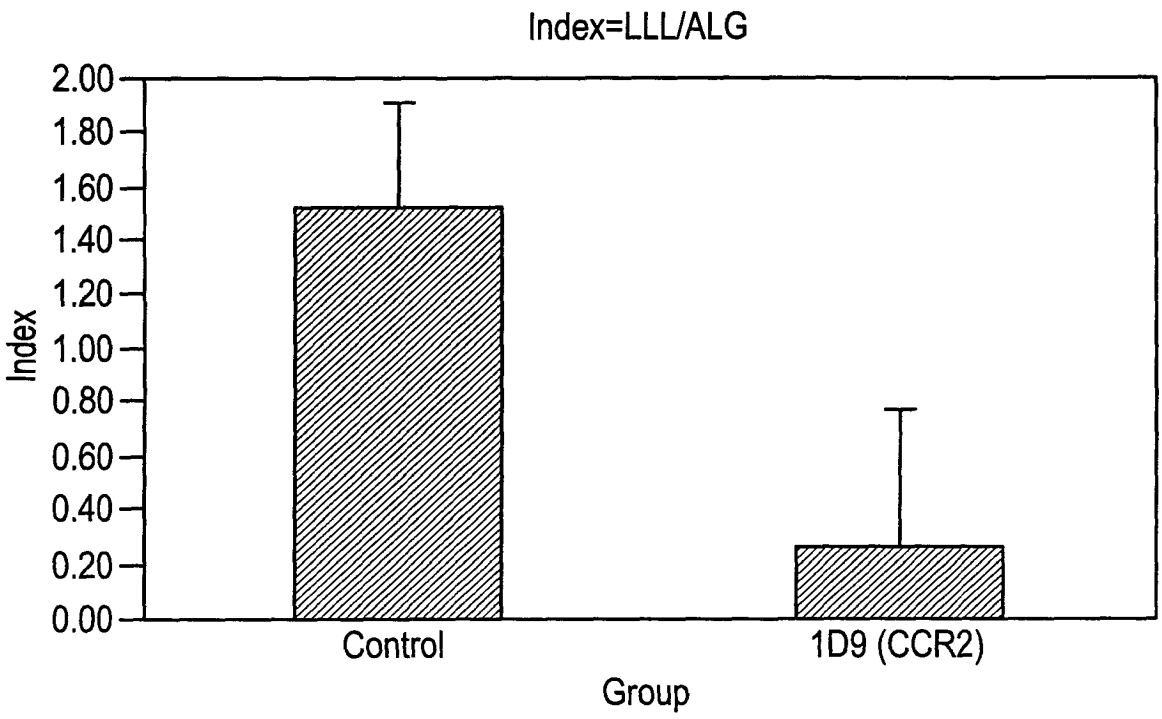

Index=LLL/ALG
2.00
1.80
1.60
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
Index
Control
1D9 (CCR2)
Group

FIG. 5D

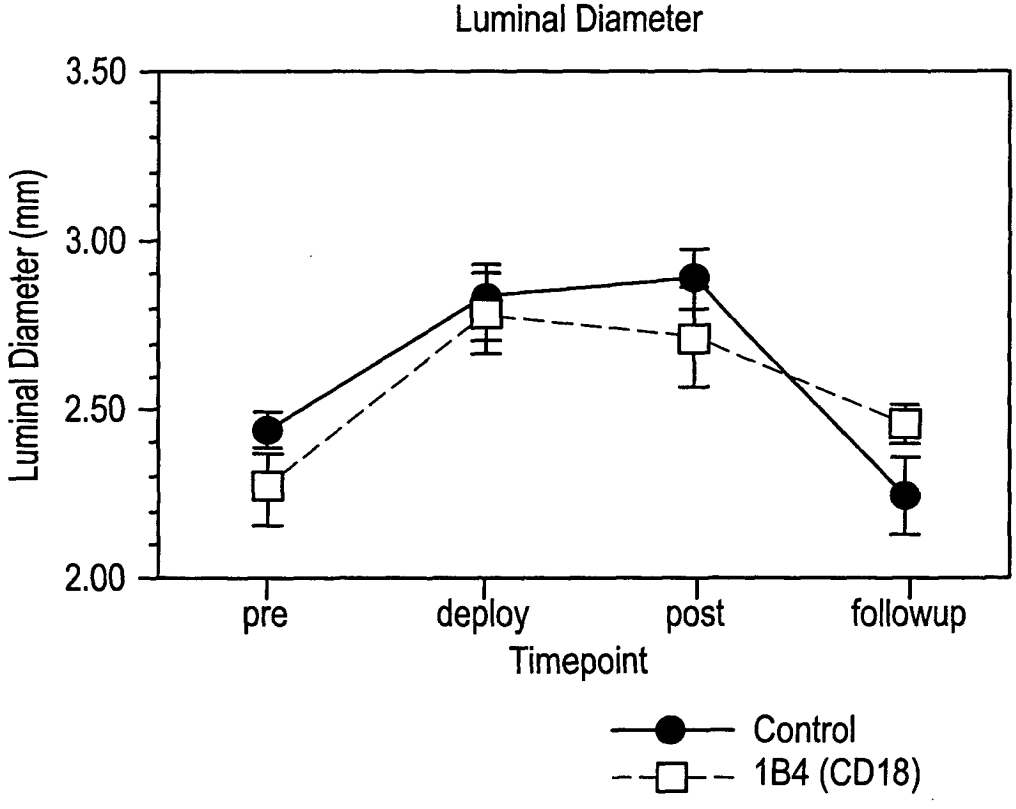

Luminal Diameter
3.50
3.00
2.50
2.00
Luminal Diameter (mm)
pre
deploy
post
followup
Timepoint
Control
1B4 (CD18)

FIG. 5E

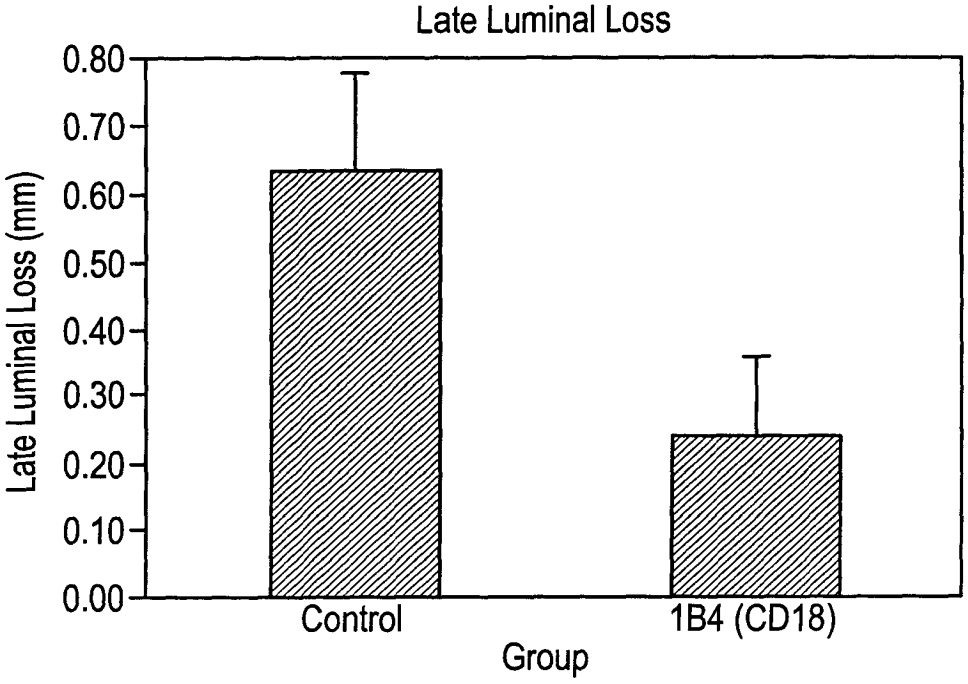

Late Luminal Loss
Late Luminal Loss (mm)
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
Control
1B4 (CD18)
Group

FIG. 5F

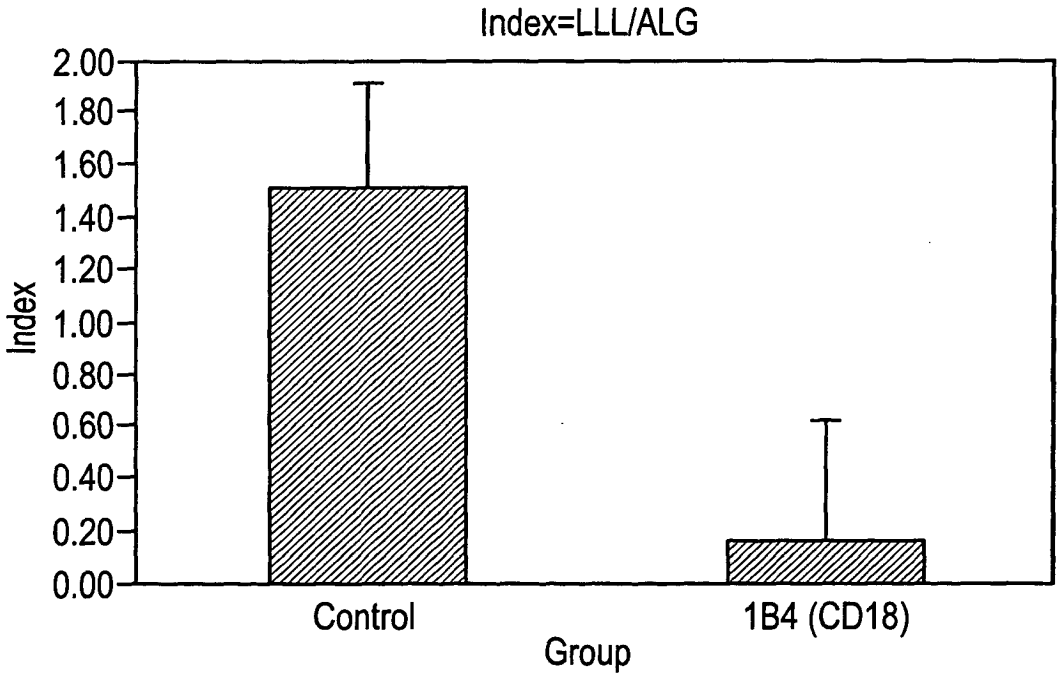

Index=LLL/ALG
Index
2.00
1.80
1.60
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
Control
1B4 (CD18)
Group

FIG. 6A

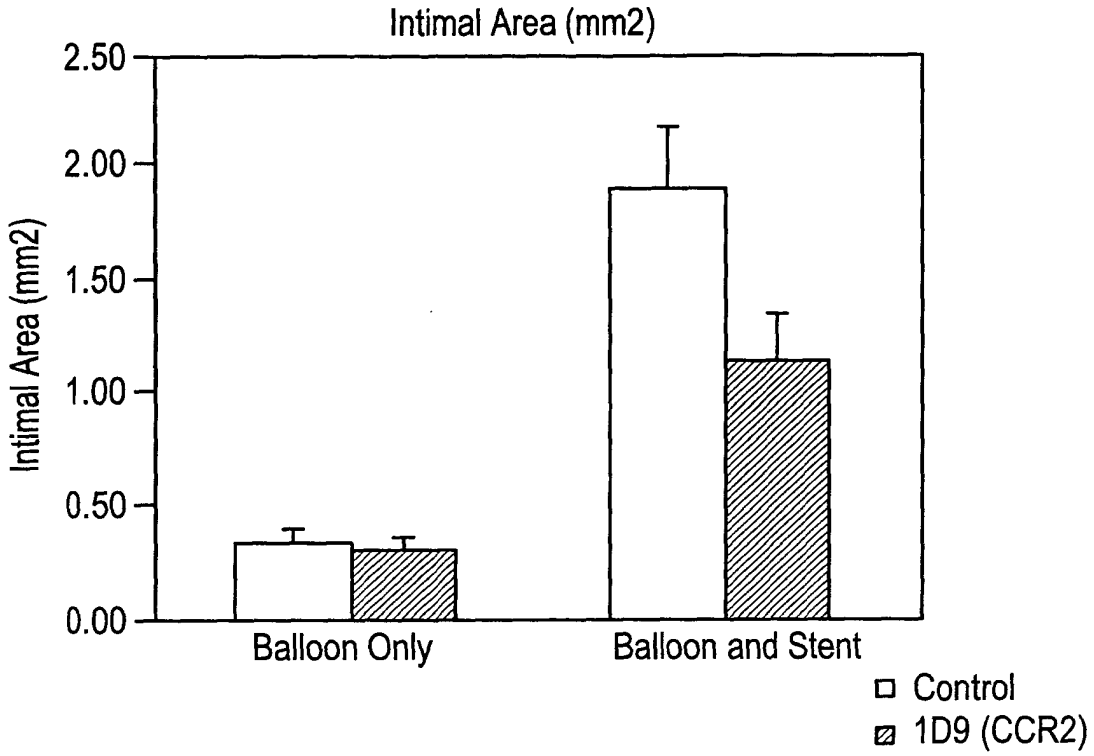

Intimal Area (mm2)
2.50
2.00
1.50
1.00
0.50
0.00
Intimal Area (mm2)
Balloon Only
Balloon and Stent
Control
1D9 (CCR2)

FIG. 6B

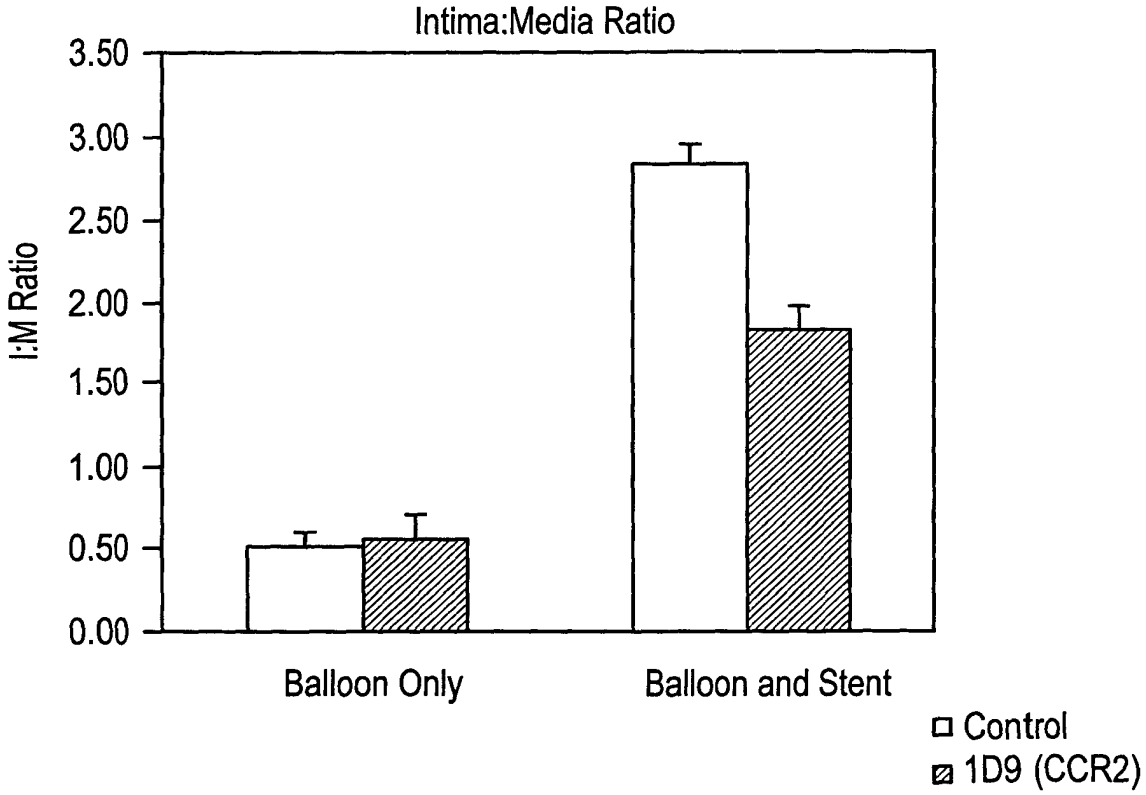

Intima:Media Ratio
3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
I:M Ratio
Balloon Only
Balloon and Stent
Control
1D9 (CCR2)

FIG. 6C

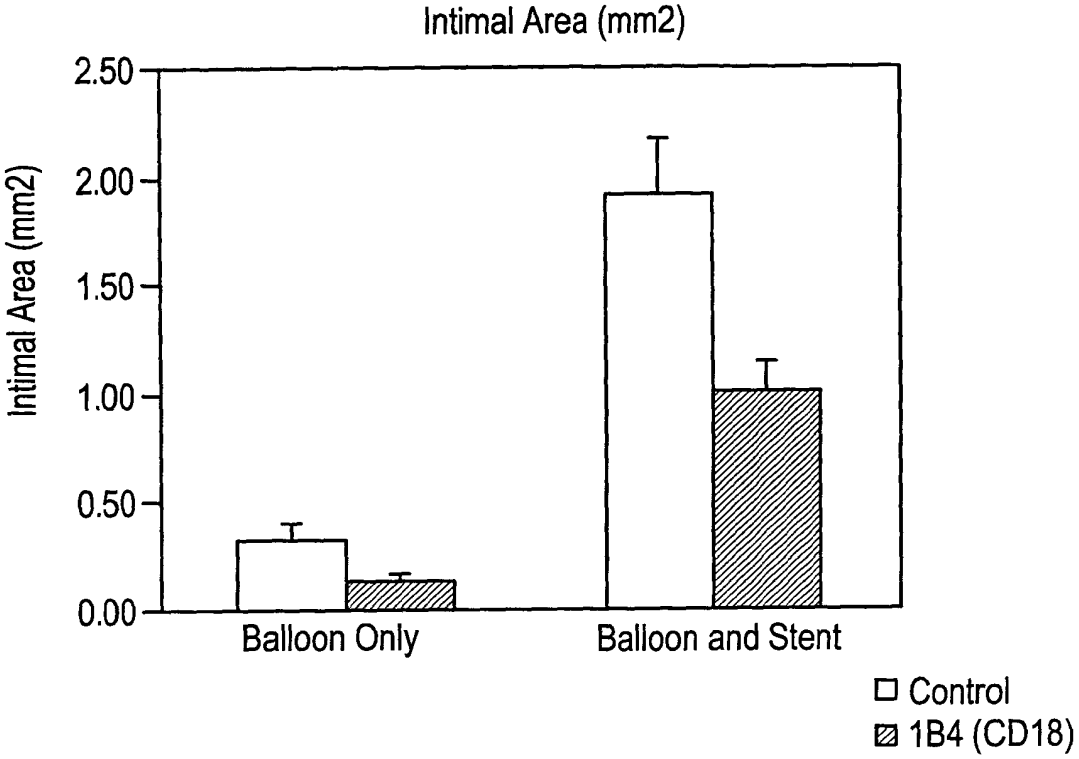
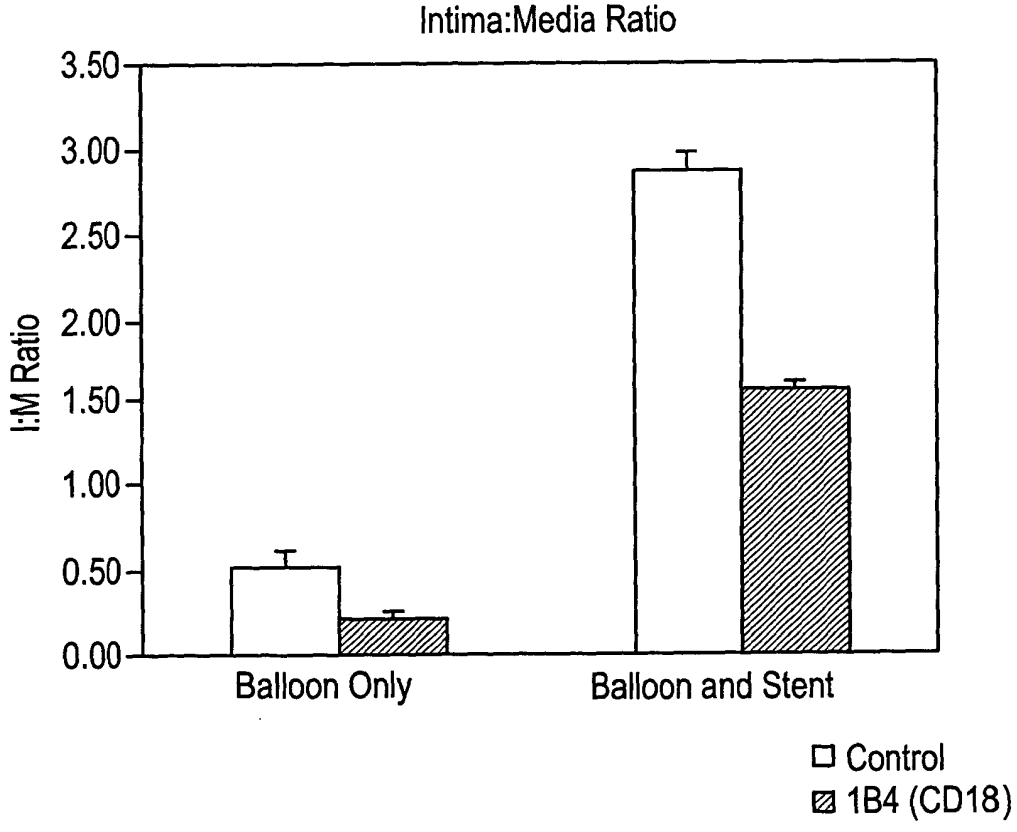

Intimal Area (mm2)
Intimal Area (mm2)
2.50
2.00
1.50
1.00
0.50
0.00
Balloon Only
Balloon and Stent
Control
1B4 (CD18)

FIG. 6D


Intima:Media Ratio
I:M Ratio
3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
Balloon Only
Balloon and Stent
Control
1B4 (CD18)

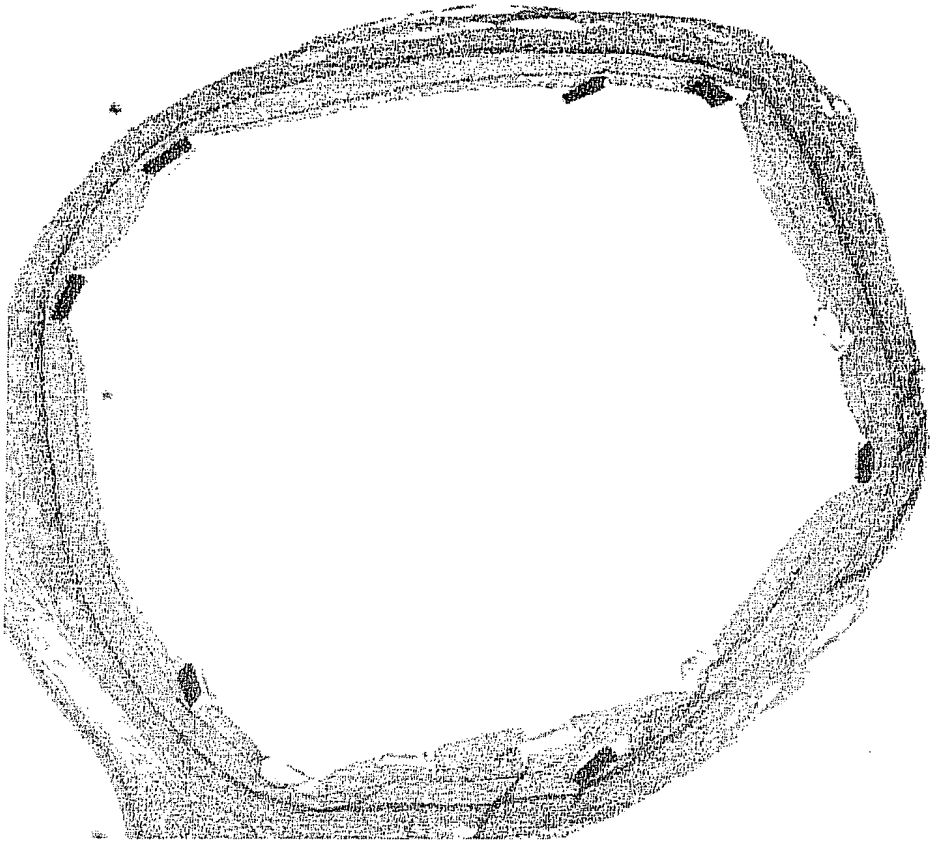


Fig. 7B

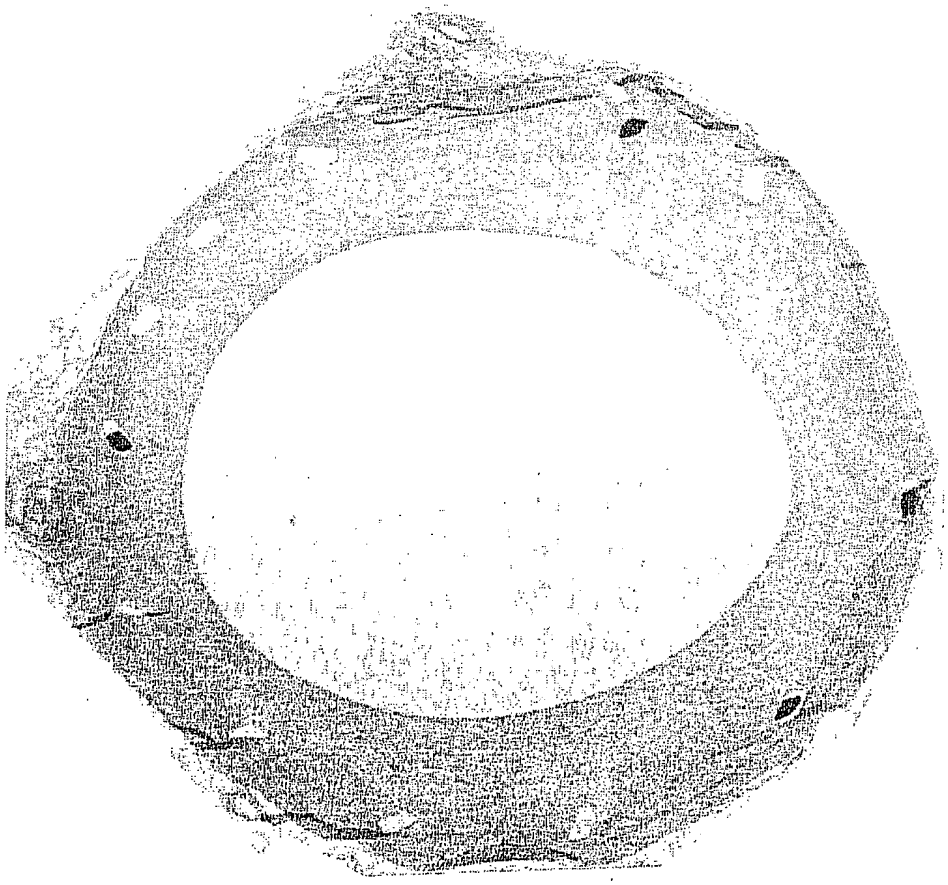


Fig. 7A

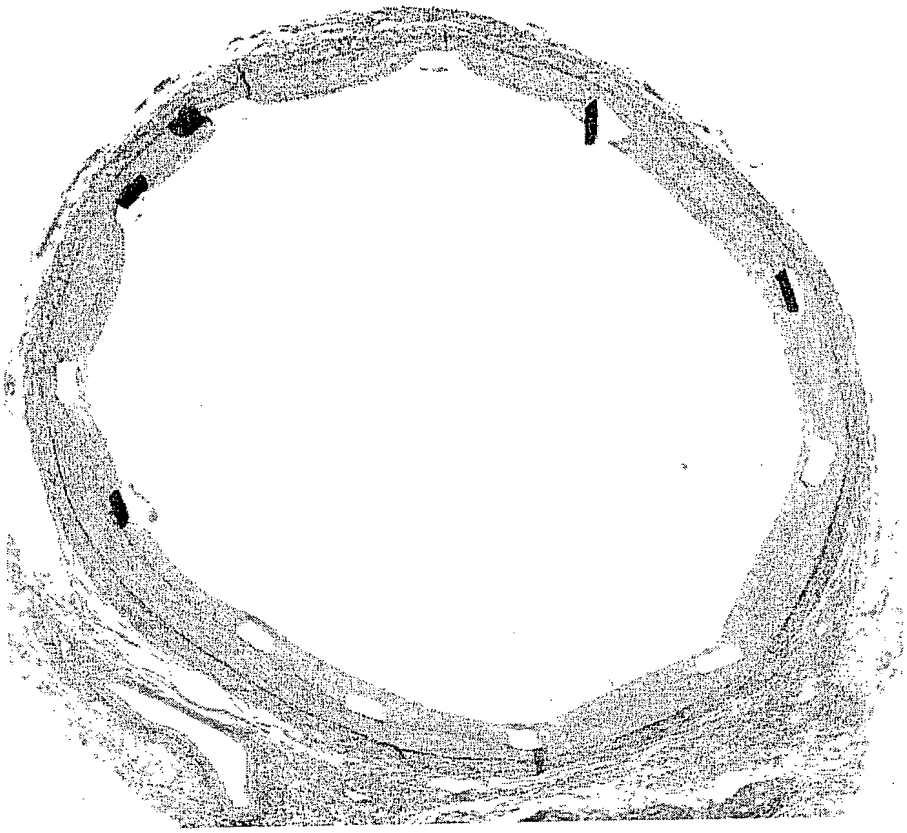


Fig. 8B

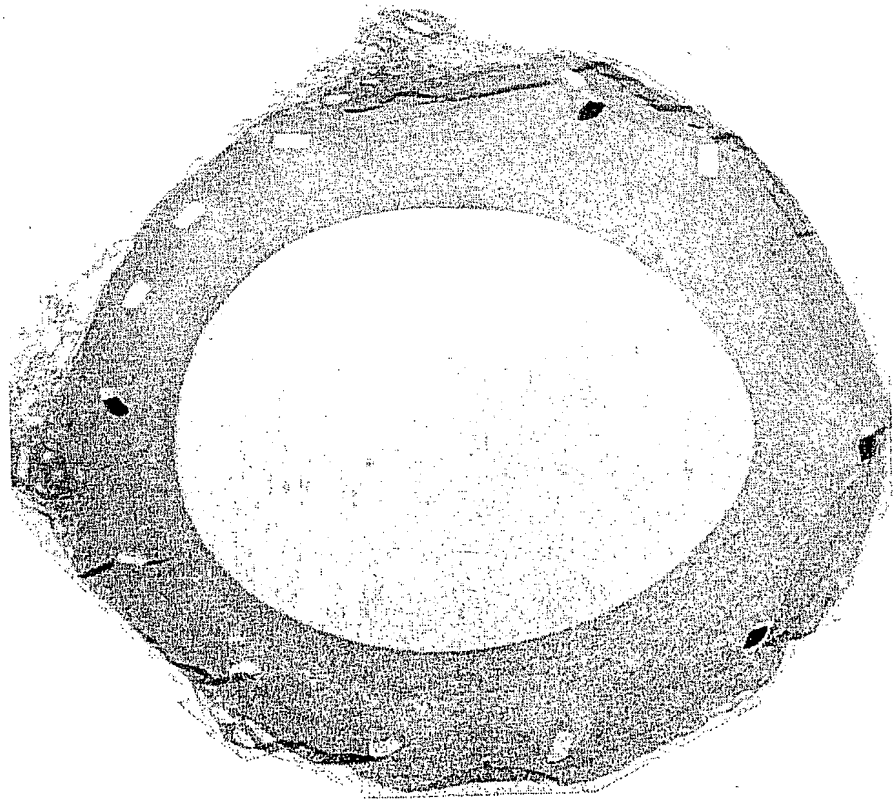


Fig. 8A

Met Arg Val Gln Val Gln Phe Leu Gly Leu Leu Leu Leu Trp Thr Ser

Gly Ala Gln Cys Asp Val Gln Met Thr Gln Ser Pro Ser Tyr Leu Ala

Ala Ser Pro Gly Glu Ser Val Ser Ile Ser Cys Lys Ala Ser Lys Ser

Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Glu Ala Asn

Lys Leu Leu Val Tyr Tyr Gly Ser Thr Leu Arg Ser Gly Ile Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg

Asn Leu Glu Pro Ala Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr

Glu Arg Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu

Fig. 9

CDR1	Lys Ala Ser Lys Ser Ile Ser Asn Tyr Leu Ala
CDR2	Tyr Gly Ser Thr Leu Arg Ser
CDR3	Gln Gln Tyr Tyr Glu Arg Pro Leu Thr

Fig. 10

Met Lys Cys Ser Trp Ile Asn Leu Phe Leu Met Ala Leu Ala Ser Gly

Val Tyr Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Arg Arg

Pro Gly Ser Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ser Ile

Lys Asp Tyr Leu Leu His Trp Val Lys His Arg Pro Glu Tyr Gly Leu

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Gly

Gln Lys Phe Gln Ser Arg Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Thr

Tyr Phe Cys Thr Arg Gly Glu Tyr Arg Tyr Asn Ser Trp Phe Asp Tyr

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

Fig. 11

CDR1	Asp Tyr Leu Leu His
CDR2	Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Gly Gln Lys Phe Gln Ser
CDR3	Gly Glu Tyr Arg Tyr Asn Ser Trp Phe Asp Tyr

Fig. 12

1 MGWSCIILFL VATATGVHSQ VQLQESGPGL VRPSQTLSLT CTVSGFTFTD

51 YLLHWVRQPP GRGLEWIGWI DPEDGETKYG QKFQSRVTML VDTSKNQFSL

101 RLSSVTAADT AVYYCARGEY RYNSWFDYWG QGSLVTVSS

Fig. 13

1 MGWSCIILFL VATATGVHSD IQMTQSPSSL SASVGDRVTI TCKASKSISN

51 YLAWYQQKPG KAPKLLIYYG STLRSGVPSR FSGSGSGTDF TFTISSLQPE

101 DIATYYCQQY YERPLTFGQG TKVEIKR

Fig. 14

```
  1  DVVMTQTPLT LSVTVGHPAS ISCKSSQSLL DSDGKTFLNW LLQRPGQSPK

 51  RLIYLVSKLD SGVPDRFTGS GSGTDFTLKI SRVEAEDLGV YYCWQGTHFP

101  YTFGGGTKLE IK
```

Fig. 15

```
  1  EVQLVESGGG LVQPKGSLKL SCAASGFSFN AYAMNWVRQA PGKGLEWVAR

 51  IRTKNNNYAT YYADSVKDRY TISRDDSESM LFLQMNNLKT EDTAMYYCVT

101  FYGNGVWGTG TTVTVSS
```

Fig. 16

```
CDRs                              =======L1========          ==L2===                    ======L3=======

Kabat Numbers                                                                                          1
                    1         2         3         4         5         6         7         8         9         0
          12345678901234567890123456ABCDEF8901234567890123456789012345678901234567890123456789012345678901234ABCDEF67890123456A7

1D9 V_K   DVVMTQTPLTLSVTVGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP------YTFGGGTKLEI-K

HF-21/28 V_K ......S..S.P..L.Q......R.....VH. ..N.Y...FQ.......R....K..NR........S.....................V.....M....W.       F...Q..R...

1D9RK_A V_K   DVVMTQSPLSLPVTLGQPASISCKSSQSLLDS-DGKTFLNWFQQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGQGTRLEI-K

1D9RK_B V_K   DVVMTQSPLSLPVTLGQPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGQGTRLEI-K

1D9RK_C V_K   DVVMTQSPLSLPVTLGQPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGGGTRLEI-K

1D9RK_D V_K   DVVMTQSPLSLPVTLGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGGGTRLEI-K

1D9RK_E V_K   DVVMTQSPLSLPVTLGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGQGTRLEI-K
```

Key

1D9 V_K	Mouse 1D9 V_K region
HF-21/28 V_K	Chosen human framework acceptor V_K region sequence with mismatches to the 1D9 V_K region highlighted.
1D9RK$_A$ V_K	CDR grafted 1D9 V_K region, with no back mutations but with the added human lysine residue at position 107 (i.e., 107K).
1D9RK$_B$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L and Q37L, and the additional 107K insertion.
1D9RK$_C$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L, Q37L and Q100G, and the additional 107K insertion.
1D9RK$_D$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L, Q37L, Q100G and Q17H, and the additional 107K insertion.
1D9RK$_E$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L, Q37L and Q17H, and the additional 107K insertion.

Fig. 17

```
CDRs                                   -----==H1===            =========H2========                                         ======H3=======

Kabat Numbers                                                                                                                     1                1
            1         2         3           4         5            6         7         8            9         0                1
   12345678901234567890123456789012345AB678901234567890123ABC34567890123456789012345678901234ABC34567890123456789012345678901234567890ABC-IJK1234567890123

1D9
   EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSESMLFLQMNNLKTEDTAMYYCVTFYGN--------GVWGTGTTVTVSS

4B4'CL VH
   ............K.G...R.......T.SNAW.S  .............G..KS.TDGGT.D..AP..G.F.......KNT.Y....S.......V...T.DSLPPH        R...Q..L.....

1D9RHA VH
   EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMN--WVRQAPGKGLEWVGRIRTKNNNYATYYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGN---------GVWGQGTLVTVSS

1D9RHB VH
   EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVGRIRTKNNNYATYYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGN---------GVWGQGTLVTVSS

1D9RHC VH
   EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGN---------GVWGQGTLVTVSS

1D9RHD VH
   EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSKNTLYLQMNSLKTEDTAVYYCVTFYGN---------GVWGQGTLVTVSS
```

Key

1D9 V_H	Mouse 1D9 V_H region.
4B4'CL V_H	Chosen human framework acceptor V_H region sequence with mismatches to the 1D9 V_H region highlighted.
1D9RH$_A$ V_H	CDR grafted 1D9 V_H region, with no back mutations.
1D9RH$_B$ V_H	CDR grafted 1D9 V_H region, with back mutations at T28S and S30N.
1D9RH$_C$ V_H	CDR grafted 1D9 V_H region, with back mutations at T28S, S30N, G49A and F67Y.
1D9RH$_D$ V_H	CDR grafted 1D9 V_H region, with back mutations at T28S, S30N, G49A, F67Y and T93V.

Fig. 18